

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2001, 15:46:56 ; Search time 210.42 Seconds
(without alignments)
7.313 Million cell updates/sec

Title: US-09-331-631A-1_COPY_29_73
Perfect score: 252
Sequence: 1 SEFDROXYECKRQCQMLET.....RCVSQCDKRFEDIDMSKYD 45

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_36:*

- 1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:*
- 2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT:*
- 6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT:*
- 7: /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT:*
- 8: /SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT:*
- 9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT:*
- 10: /SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT:*
- 11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT:*
- 12: /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT:*
- 13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT:*
- 17: /SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT:*
- 18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	252	100.0	666	19 W62828	Macadamia integrif
2	252	100.0	666	19 W62829	Macadamia integrif
3	180	71.4	625	19 W62830	Macadamia integrif
4	78.5	31.2	590	19 W62832	Gossypium hirsutum
5	70.5	28.0	525	19 W62831	Theobroma cacao an
6	70.5	28.0	566	13 R20181	Sequence encoded b
7	67	26.6	218	19 W40287	Human TSP1 protein
8	67	26.6	218	20 Y06182	Thrombospondin I f
9	67	26.6	239	14 R40823	Human thrombospond
10	67	26.6	441	19 W40288	Human concatamers
11	67	26.6	441	20 Y06183	Thrombospondin I f
12	63	25.0	444	20 W90340	G. max truncated S

13	63	25.0	524	20 W90339	G. max SBP1 protei
14	62.5	24.8	409	20 W90342	G. max truncated S
15	62.5	24.8	489	20 W90341	G. max SBP2 protei
16	62	24.6	941	21 Y66736	Membrane-bound pro
17	59.5	23.6	2703	16 R70236	P. falciparum Proj
18	59.5	23.6	2710	18 W22482	Plasmodium Proj3.
19	59.5	23.6	2710	21 Y77904	P. falciparum Proj
20	59.5	23.6	3060	18 W22475	Plasmodium var-7.
21	59.5	23.6	3060	21 Y77905	Plasmodium var-7 p
22	57	22.6	1284	9 P81187	Sequence encoded b
23	56.5	22.4	593	19 W62835	Zea mays antimicro
24	55	21.8	623	20 W30622	Arabidopsis enhanc
25	55	21.8	816	16 R85870	WD-40 domain-contg
26	53.5	21.2	450	19 W56779	Human beclin prote
27	53.5	21.2	450	19 W56784	Human beclin prote
28	53	21.0	35	13 R21079	Antimicrobial maiz
29	52.5	20.8	569	20 Y24054	A human beta-trans
30	52.5	20.8	569	21 Y83041	F-box protein FBP-
31	52.5	20.8	569	21 Y83250	F-box protein hbet
32	52.5	20.8	569	21 Y44249	Human cell signal
33	52	20.6	33	19 W62836	Zea mays antimicro
34	52	20.6	58	20 Y32115	Maize id gene NsII
35	52	20.6	436	20 Y32114	Maize id protein.
36	52	20.6	623	20 W30620	Arabidopsis La-er
37	52	20.6	623	20 W30624	Arabidopsis mutant
38	51.5	20.4	147	13 R22950	Leech antiplatelet
39	51.5	20.4	569	21 Y83254	F-box protein FWD1
40	51.5	20.4	5250	21 Y53678	Sequence g1/442661
41	49.5	19.6	98	17 R91700	AcANP6. Ancylost
42	49.5	19.6	98	20 Y30395	Nematode extracted
43	49.5	19.6	562	18 W12096	Adenovirus E1a ass
44	49	19.4	411	21 Y77914	Plasmodium DBL gen
45	49	19.4	467	21 Y70814	Extended human zsl

ALIGNMENTS

RESULT 1	W62828	standard; Protein; 666 AA.
ID	W62828	
XX	W62828;	
AC	XX	
XX	XX	
DT	27-OCF-1998	(first entry)
XX	XX	
DE	Macadamia integrifolia antimicrobial protein.	
XX	XX	
KW	antimicrobial protein; infestation; control.	
XX	XX	
OS	Macadamia integrifolia.	
XX	XX	
FH	Key	Location/Qualifiers
FT	Peptide	1..28
FT	Protein	/note="signal peptide"
FT		29..666
FT		/note="mature protein"
XX	XX	
PN	W09827805-A1.	
XX	XX	
PD	02-JUL-1998.	
XX	XX	
PF	22-DEC-1997:	97WO-AU00874.
XX	XX	
PR	20-DEC-1996:	96AU-0004275.
XX	XX	
PA	(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.	
XX	XX	
PI	Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP:	
XX	XX	
DR	WPI: 1998-377279/32.	
DR	N-PSDB: V42310.	
XX	XX	

PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
XX useful for controlling microbial infestations of plants or mammals
XX
PS Claim 1; Page 34-36; 96pp; English.
XX
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
XX
SO Sequence 666 AA;

Query Match 100.0%; Score 252; DB 19; Length 666;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEPDRQYECKRCQCMQLETSQGMRCVSOCDKRFEDIDWSKYD 45
Db 29 sefdrgyeckrqcmqltsqgmrcvsgcdkrfeedidwskyd 73

RESULT 2
W62829 ID W62829 standard; Protein; 666 AA.
AC W62829;
XX
DT 27-OCT-1998 (first entry)
XX
DE Macadamia integrifolia antimicrobial protein.
XX
KM antimicrobial protein; infestation; control.
XX
OS Macadamia integrifolia.
XX
FH Key Location/Qualifiers
FT Peptide 1..28 /note= "signal peptide"
FT Protein 29..666 /note= "mature protein"
XX
PN MO9827805-A1.
XX
PD 02-JUL-1998.
XX
PF 22-DEC-1997; 97WO-AU00874.
XX
PR 20-DEC-1996; 96AU-0004275.
XX
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
XX
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
XX
DR WPI; 1998-377279/32.
XX
DR N-PSDB; V42311.
XX
XX Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
XX
PS Claim 1; Page 39-41; 96pp; English.
XX
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
XX
SO Sequence 666 AA;

Query Match 100.0%; Score 252; DB 19; Length 666;
Best Local Similarity 100.0%; Pred. No. 2.3e-23;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEPDRQYECKRCQCMQLETSQGMRCVSOCDKRFEDIDWSKYD 45

Db 29 sefdrgyeckrqcmqltsqgmrcvsgcdkrfeedidwskyd 73

RESULT 3
W62830 ID W62830 standard; Protein; 625 AA.
XX
AC W62830;
XX
DT 27-OCT-1998 (first entry)
XX
DE Macadamia integrifolia antimicrobial protein.
XX
KM antimicrobial protein; infestation; control.
XX
OS Macadamia integrifolia.
XX
FH Key Location/Qualifiers
FT Peptide 1..28 /note= "signal peptide"
FT Protein 29..666 /note= "mature protein"
XX
PN MO9827805-A1.
XX
PD 02-JUL-1998.
XX
PF 22-DEC-1997; 97WO-AU00874.
XX
PR 20-DEC-1996; 96AU-0004275.
XX
PA (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
XX
PI Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
XX
DR WPI; 1998-377279/32.
XX
DR N-PSDB; V42316.
XX
PT Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
XX
PS Claim 1; Page 43-45; 96pp; English.
XX
CC The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
XX
SO Sequence 625 AA;

Query Match 71.4%; Score 180; DB 19; Length 625;
Best Local Similarity 100.0%; Pred. No. 1.7e-14;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 QCMQLETSQGMRCVSOCDKRFEDIDWSKYD 45
Db 1 qcmqltsqgmrcvsgcdkrfeedidwskyd 32

RESULT 4
W62832 ID W62832 standard; Protein; 590 AA.
XX
AC W62832;
XX
DT 27-OCT-1998 (first entry)
XX
DE Gossypium hirsutum antimicrobial protein.
XX
KM antimicrobial protein; infestation; control.
XX
OS Gossypium hirsutum.

XX WO9827805-A1.
PN
XX
PD 02-JUL-1998.
XX
XX 22-DEC-1997; 97WO-AU00874.
PF
XX 20-DEC-1996; 96AU-0004275.
PR
XX (RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.
PA
XX Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;
PI
XX WPI; 1998-377279/32.
DR
XX
XX Novel anti-microbial protein from e.g. Macadamia integrifolia -
PT useful for controlling microbial infestations of plants or mammals
PP
XX
PS Claim 1; Page 49-51; 96pp; English.
XX
XX The sequence is that of an antimicrobial protein which can
CC be used to control microbial infestations in plants and mammalian
CC animals.
XX
SQ Sequence 590 AA;

Query Match	31.2%	Score 78.5	DB 19	Length 590
Best Local Similarity	40.5%	Pred. 0.055		
Matches	15	Conservative	9	Mismatches 12
				Indels 1
				Gaps 1
QY	2	EFDRQVEYECRQCMQETSGOMRRCVSCQCKRFEED	38	
	↓	::: :::	↓	::: :::
Db	81	edppriyeeeqecqeqe-erqapqpcqrcklkrifee	116	

XX	RESULT	5	
XX	ID	W62831	
XX	AC	W62831 standard; Protein; 525 AA.	
XX	XX	W62831;	
XX	DT	27-OCT-1998 (first entry)	
XX	DE	Theobroma cacao antimicrobial protein.	
XX	KW	antimicrobial protein; infestation; control.	
XX	XX	Theobroma cacao.	
XX	OS		
XX	PN	W09827805-A1.	
XX	PD	02-JUL-1998.	
XX	PF	22-DEC-1997; 97WO-AU00874.	
XX	PR	20-DEC-1996; 96AU-0004275.	
XX	PA	(RETR-) COOP RES CENT TROPICAL PLANT PATHOLOGY.	
XX	PI	Bower NI, Goulter KC, Green JL, Manners JM, Marcus JP;	
XX	DR	WPI; 1998-377279/32.	
XX	PT	Novel anti-microbial protein from e.g. Macadamia integrifolia -	
XX	PS	useful for controlling microbial infestations of plants or mammals	
XX	CC	Claim 1; Page 47-49; 96pp; English.	
XX	CC	The sequence is that of an antimicrobial protein which can	
XX	CC	be used to control microbial infestations in plants and mammalian	
XX	XX	animals.	

SQ	Sequence	525 AA;
	Query Match	28.0%, Score 70.5; DB 19; Length 525; Best Local Similarity 32.4%; Pred. No. 0.47;
OY	Matches	11; Conservative 11; Mismatches 11; Indels 1; Gaps 1;
D6		5 ROEYECKRQCQLLET-SGOMRRCVSODDKREE 37 :: :: :: :: :: :: 39 rgyegcqqrccseateeregeqcccqrteerkyke 72

	RESULT	6
XX	ID	R20181
XX		R20181 standard; Protein; 566 AA.
XX	AC	R20181;
XX	DT	16-APR-1992 (first entry)
XX		Sequence encoded by 67 kD T. cacao protein cDNA.
XX		Cocoa, flavour; vicilin; seed storage protein..
XX	OS	Theobroma cacao.
XX	PN	WO9119801-A.
XX	PD	26-DEC-1991.
XX		07-JUN-1991; 91WO-GB00914.
XX	PF	11-JUN-1990; 90GB-0013016.
XX	PR	(MIRC) MARS UK LTD.
XX	PA	Spencer ME, Hodge R, Deakin EA, Ashton S;
XX	P1	WPI; 1992-024418/03.
XX	DR	N-PDB; Q20377.
XX		Recombinant cocoa proteins - are responsible for flavour in cocoa beans and produced in large quantities using yeast and bacterial expression vectors
PT		Claim 4; Fig 2; 59pp; English.
PS		The inventors claim a 67 kD and 31 kD T. cacao protein, and
CC		fragments, and encoding DNAs. The 47 kD and 31 kD proteins are
CC		derived from the 67 kD precursor. T. cacao protein cDNA was
CC		detected in a cDNA library prepared from immature cocoa beans RNA
CC		using a probe based on the AA sequence of a CNBR peptide common to
CC		the 47 kD and 31 kD polypeptides. Homology searches revealed close
CC		homologies between the 67 kD polypeptide and the vicilins, which are
CC		seed storage proteins.
XX		Sequence 566 AA.
XQ		

Query Match	28.0% ;	Score 70.5 ;	DB 13 ;	Length 566 ;
Best Local Similarity	32.4% ;	Pred. No. 0.51 ;		
Matches 11 ;	Conservative 11 ;	Mismatches 11 ;	Indels 1 ;	Gaps 1 ;
OY	5	ROEYEECKRQOCMOLET-SGOMRRCVSQCCKRFEF	37	
	11:11:11:11	1	:	1:1:1:1
			:	1:1:1:1
Db	39	rgygeqqrceateeregeqceqrereyke	72	
RESULT	7			
W40287				
ID	W40287	standard:	Protein, 218 AA.	
XX				
XC	W40287;			

xx	18-AUG-1998	(first entry)
DF		
xx		
DE		Human TSPI protein.
xx		
KW	TSPI; thrombospondin; anti-angiogenic; cationic vehicle; gene therapy;	
KW	liposome; DNA complex; tumour suppressor protein; treatment; neoplastic;	
KW	metabolic disease; tumour.	
xx		
OS		Homo sapiens.
xx		
EH		
FT	Key	Location/Qualifiers
FT	Misc-difference	160
FT	/note= "encoded by CGG"	
FT	Misc-difference	217
FT	/note= "encoded by CT"	
FT	Peptide	12..27
FT	/label= anti-angiogenic peptide	
FT	Peptide	142..159
FT	/label= anti-angiogenic peptide	
FT	Peptide	199..217
FT	/label= anti-angiogenic peptide	
xx		
PN	EP819758-A2.	
xx		
PD	21-JAN-1998.	
xx		
PE	16-JUL-1997;	97EP-0112154.
xx		
PR	16-JUL-1996;	96US-0680845.
xx		
PA	(MIXS/) MIXSON A J.	
xx		
PI	Mixson AJ;	
xx		
DR	WPI; 1998-078839/08.	
xx		
DR	N-PSDB; V10493.	
xx		
PT	Complexes of DNA encoding anti-angiogenic peptide - with cationic	
PT	liposome(s) or cationic polymer, useful for, e.g. gene therapy of	
xx	tumours	
PS		
xx		
PS	Claim 9; Page 6; 47pp; English.	
xx		
CC	This sequence represents the thrombospondin gene TSPI which is used	
CC	in a method to produce a cationic vehicle consisting of a cationic	
CC	liposome:DNA complex where the DNA encodes an anti-angiogenic peptide or	
CC	tumour suppressor protein. Such complexes are used for treatment of	
CC	neoplastic and metabolic diseases especially for gene therapy of tumours.	
xx		
SO	Sequence	218 AA;
Query Match	26.6%;	Score 67; DB 19; Length 218;
Best Local Similarity	39.5%;	Pred. No. 0.49;
Matches	15; Conservative	6; Mismatches 11; Indels 6; Gaps 2
QY	13 ROCMOLE-----TSCOMRRC-VSCDCKREEDIDMSKY	44
	: : :	
DB	104 tscdslnnrcegssvqltchiquecdkrfkgdgwshw	141
RESULT	8	
Y06182	Y06182 standard; Protein; 218 AA.	
xx		
AC	Y06182;	
xx		
DT	16-AUG-1999 (first entry)	
xx		
DE	Thrombospondin I fragment.	
xx		
xx	Anti-angiogenic; carrier:DNA complex; tumour; gene therapy; human;	

KM		Chromospondin I; melanoma; lung cancer; colon cancer;
KM		brain cancer; breast cancer.
XX		
OS	Homo sapiens.	
FH	Key	Location/Qualifiers
FT	Misc-difference 160	/note= "encoded by CCG"
FT	Misc-difference 161	/note= "encoded by CTC"
FT	Misc-difference 162	/note= "encoded by TGC"
FT	Misc-difference 163	/note= "encoded by AAC"
FT	Misc-difference 177	/note= "encoded by GAA"
FT	Misc-difference 178	/note= "encoded by GCG"
FT	Misc-difference 179	/note= "encoded by CGG"
XX		
PN	EP921193-A1.	
PD	09-JUN-1999.	
XX		
PF	07-JAN-1998;	98EP-0100135.
XX		
PR	05-DEC-1997;	97US-0985526.
XX		
PA	(MIXS/) MIXSON A J.	
XX		
PI	Mixson AJ;	
DR	WPI; 1999-315406/27.	
DR	N-PSDB; X58725.	
XX		
PT	Inhibition of growth of solid tumors	
XX		
PS	Disclosure; Page 17-18; 46pp; English.	
XX		
CC	This sequence represents an anti-angiogenic fragment of the	
CC	thrombospondin I protein. The invention provides a carrier:DNA	
CC	complex that comprises DNA (see X58725-42) coding for an	
CC	anti-angiogenic protein or peptide, the complex being deliverable	
CC	to the site of a tumour in vivo, and which additionally comprises	
CC	regulatory elements for expressing the anti-angiogenic DNA in a	
CC	tumour or tumour vasculature. The complex may also include DNA	
CC	encoding a tumour suppressor protein, especially p53. The carrier	
CC	is a liposome, cationic polymer, micelle, microsphere, virus, viral	
CC	component, or a combination of these, and administration is by	
CC	intravenous or intratumoral injection. The complexes are useful in	
CC	gene therapy for inhibition of tumour growth. The types of tumors	
CC	which may be treated include solid tumors such as melanomas and	
CC	tumors in the lung, colon, brain and breast.	
XX		
SQ	Sequence	218 AA;
<hr/>		
Query Match	26.6%;	Score 67; DB 20; Length 218;
Best Local Similarity	39.5%;	Pred.No. 0.49;
Matches 15; Conservative	6;	Mismatches 11; Indels 6; Gaps 2;
<hr/>		
QY	13 RCGMLE-----TSCOMRRC-VSCCDKRFEEIDISKY 44	
	: : : :	
Db	104 rscdslnrcegssvqtrchqecdkrfkgdgswhw 141	
<hr/>		
RESULT	9	
ID	R40823 standard; protein; 239 AA.	
NC	R40823;	
XX		

DT	03-MAR-1994	(first entry)
XX		
DE	Human thrombospondin 1.	
XX		
KW	hTSP-1; platelet glycoprotein; angiogenesis; neovascularisation; inhibitor; solid tumour; skin cancer; angiogenic dysfunction; melanoma; diabetic retinopathy; psoriasis; neovascular glaucoma; Kaposi's sarcoma; inflammation; retrolental fibroplasia.	
XX		
OS	Homo sapiens.	
XX		
PN	W09316716-A.	
XX		
PD	02-SEP-1993.	
XX		
PF	22-FEB-1993; 93WO-US01652.	
XX		
PR	24-FEB-1992; 92US-0841656.	
XX		
PA	(NOUN) UNIV NORTHWESTERN.	
XX		
PI	Bouck NP, Frazier WA, Good DJ, Polverini PJ;	
DR	WPL: 1993-288118/36.	
XX		
XX		
PT	Compn. for inhibiting angiogenesis - contg. a vascularisation inhibitor comprising a peptide capable of inhibiting vascularisation	
PS	Claim 10; Page 41-42; 51pp: English.	
XX		
CC	Certain fragments of thrombospondin, a glycoprotein found in the alpha granules of platelets, can inhibit vascularisation. Peptides derived from the hTSP sequence are useful for inhibiting neovascularisation, esp. in solid tumours such as melanomas. The inhibitory peptides can also be used in other diseases involving angiogenic dysfunction. See R40824-R40830.	
CC		
XX		
SQ	Sequence 239 AA;	
Query Match 26.6%; Score 67; DB 14; Length 239;		
Best Local Similarity 39.5%; Pred. No. 0.54;		
Matches 15; Conservative 6; Mismatches 11; Indels 6; Gaps 2;		
QY	13 ROCMOLE-----TSGQMRRC-VSCQDKRFEEEDIMSKY 44	
	: : :	
DB	93 rtscdslmrccsgsvqrtrchqecdkrfkdgsgwshw 130	
RESULT 10		
WA0288		
ID	WA0288 standard; Protein; 441 AA.	
XX		
AC	WA0288;	
XX		
DT	18-AUG-1998 (first entry)	
XX		
DE	Human concatamerised TSP1 protein.	
XX		
KW	TSP1; thrombospondin; anti-angiogenic; cationic vehicle; gene therapy; liposome; DNA complex; tumour suppressor protein; treatment; neoplastic; metabolic disease; concatamer; tumour.	
XX		
OS	Homo sapiens.	
OS	Synthetic.	
XX		
XX		
FH	Key Location/Qualifiers	
FT	Misc-difference 160	
FT	Misc-difference 221	
FT	Misc-difference 383	
FT	Misc-difference 383	

FT		/note= "encoded by CCG"
FT	Region	223...227
FT		/label= Intervening sequence
XX		
PV	EP819758-A2.	
XX		
PD	21-JAN-1998.	
XX		
PF	16-JUL-1997;	97EP-0112154.
XX		
PR	16-JUL-1996;	96US-0680845.
XX		
PA	(MIXS/) MIXSON A J.	
XX	Mixson AJ;	
PI		
DR	WPI: 1998-078839/08.	
N-PSDB:	V10494.	
XX		
PT	Complexes of DNA encoding anti-angiogenic peptide - with cationic liposome(s) or cationic polymer, useful for, e.g. gene therapy of tumours	
PT		
PS	Claim 9; Page 6-7; 47pp; English.	
XX		
CC	This protein sequence represents a concatamer of thrombospondin TSP1 which is used in a method to produce a cationic vehicle consisting of a cationic liposome;DNA complex where the DNA encodes an anti-angiogenic peptide or tumour suppressor protein. Such complexes are used for treatment of neoplastic and metabolic diseases especially for gene therapy of tumours.	
CC		
CC		
CC		
CC		
SO	Sequence	441 AA;
QY	Query Match	26.6%; Score 67; DB 19; Length 441; Best Local Similarity 39.5%; Pred.No. 1; Matches 15; Conservative 6; Mismatches 11; Indels 6; Gaps 2;
DV	13 RQCMLF-----TSGQMRC-VSCDCKFEEDIDMSKY 44 : : : : 104 rcsdlnrcegsyvrtrchqecdkrfkdgyswsh 141	
RESULT	11	
ID	Y06183 standard; Protein; 441 AA.	
XX		
AC	Y06183;	
XX		
DT	16-AUG-1999 (first entry)	
DE	Thrombospondin I fragment concatamer.	
XX		
KW	Anti-angiogenic; carrier:DNA complex; tumour; gene therapy; human; thrombospondin I; melanoma; lung cancer; colon cancer;	
KW	brain cancer; breast cancer; concatamer.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Misc-difference 33	/note= "encoded by GTT"
FT	Misc-difference 34	/note= "encoded by GTT"
FT	Misc-difference 81	/note= "encoded by GAT"
FT	Misc-difference 81	/note= "encoded by GGC"
FT	Misc-difference 82	/note= "encoded by TGG"
FT	Misc-difference 97	/note= "encoded by AAT"
FT	Misc-difference 98	/note= "encoded by GCA"
TT		

FT	Misc-difference	160	/note=	"encoded by CGG"
FT	Misc-difference	383	/note=	"encoded by CGG"
PN	EP921193-A1.			
PD	09-JUN-1999.			
PP	07-JAN-1998:	98EP-0100135.		
PR	05-DEC-1997:	97US-0985526.		
PA	(MIXS/) MIXSON A J.			
PI	Mixson AJ:			
DR	WPI: 1999-315406/27.			
DR	N-PSDB: X58726.			
PT	Inhibition of growth of solid tumors			
PS	Disclosure: Page 19-20: 46pp; English.			
CC	The present sequence represents a concatamer of anti-angiogenic			
CC	fragments of Chromospondin 1. The invention provides a carrier:DNA			
CC	complex that comprises DNA (see X58725-42) encoding at least one			
CC	anti-angiogenic protein or peptide, the complex being deliverable			
CC	to the site of a tumour in vivo, and additionally comprises			
CC	regulatory elements for expressing the anti-angiogenic DNA in a			
CC	tumour or tumour vasculature. The complex may also include DNA			
CC	encoding a tumour suppressor protein, especially p53. The carrier			
CC	is a liposome, cationic polymer, micelle, microsphere, virus, viral			
CC	component, or a combination of these, and administration is by			
CC	intravenous or intratumoral injection. The complexes are useful in			
CC	gene therapy for inhibition of tumour growth. The types of tumors			
CC	which may be treated include solid tumors such as melanomas and			
CC	tumors in the lung, colon, brain and breast. Use of concatamers			
CC	can increase the anti-angiogenic dosage level without altering the			
CC	amount of vector necessary for delivery.			
QQ	Sequence 441 AA:			

```

Query Match          26.6%; Score 67; DB 20; Length 441;
Best Local Similarity 39.5%; Pred. No. 1;
Matches    15; Conservative    6; Mismatches   11; Indels     6; Gaps      2.

QY      13 RCGMOLF-----TSQMRRRC-VSQCDKRFEEEDIDMSKY 44
        | | | : | | : |||||::| | :
Db       104 rscdlnmrcegssvqtrtchigcdkrfkdqgyswsh 141

RESULT 12
W90340 W90340 standard; protein; 444 AA.
XX
XX W90340;
AC
XX AC
DT 24-MAY-1999 (first entry)
XX
XX DE
DE G. max truncated SBP1 protein.
XX
KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
KM seed; carbohydrate content; soybean.
XX
XX glycine max.
OS
XX OS
PN WC9853086-A1.
XX PN
PD 26-NOV-1998.
XX PD
XX 21-MAY-1998; 98WO-US10465.
XX XX

```

XX	22-MAY-1997:	97US-0047568.
XX	(UNIW)	UNIV WASHINGTON STATE RES FOUND.
XX	Chao WS,	GTimes HD;
XX	WPI;	1999-070155/06.
XX		
PT	New modified plant sucrose binding proteins -	used to develop
PT	transgenic plants which can have enhanced or	decreased sucrose
PT	uptake activity in developing seeds	
PS	Claim 7:	Page 36-37; 58pp; English.
XX		
CC	This sequence represents a novel sucrose binding protein, SBP1 isolated	
CC	from Glycine max. This protein is used in a method resulting in the	
CC	production of a modified plant sucrose binding protein (SBP) which has a	
CC	modified amino acid sequence compared to a corresponding wild-type SBP,	
CC	and where expression of the modified SBP in a yeast assay system confers	
CC	enhanced sucrose uptake compared to the corresponding wild-type SBP.	
CC	The products of the invention can be used for producing transgenic plants	
CC	which have modified sucrose uptake activity, particularly in developing	
CC	seeds. Enhanced sucrose uptake activity in developing seeds may be	
CC	desirable where it is an advantage to increase the carbohydrate content	
CC	of the seed (e.g. where the seed is the primary plant material harvested,	
CC	such as soybean). In contrast, decreased sucrose uptake activity in	
CC	seeds might be desirable where the vegetative material of the plant is	
CC	harvested. The SBP regulatory regions confer specific or enhanced	
CC	expression in developing seeds and so may be used to express any	
CC	transgene in developing seeds.	
XX		
XX	Sequence	444 AA;

Query Match	25.0%;	Score 63;	DB 20;	Length 444;
Best Local Similarity	38.2%;	Pred. No. 3.3;		
Matches 13;	Conservative	4;	Mismatches 15;	Indels 2;
			Gaps	1
2	EPDRQYECKRCRCMOLE--TSGQMRRCVSCDCK	33		
1	:	:	:	:
34	eeedpelvtckhgcqgqgyltegdkrvcqlgsedr	67		
RESULT	13			
W90339				
ID	W90339	standard; protein;	524	AA.
AC	W90339;			
XX				
DT	24-MAY-1999	(first entry)		
DE	G. max SBP1 protein.			
XX				
KM	SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;			
KM	seed; carbohydrate content; soybean.			
XX				
OS	Glycine max.			
XX				
PN	WO9853086-A1.			
XX				
PD	26-NOV-1998.			
XX				
PF	21-MAY-1998;	98WO-US10465.		
XX				
PR	22-MAY-1997;	97US-0047568.		
XX				
PA	(UNIV) UNIV WASHINGTON STATE RES FOUND.			
XX				
PI	Chao WS, Grimes HD;			
XX				
DR	WPI: 1999-070155/06.			
XX				

PT New modified plant sucrose binding proteins - used to develop
 PT transgenic plants which can have enhanced or decreased sucrose
 PT uptake activity in developing seeds
 XX
 PS Disclosure; Page 34-36; 58pp; English.
 XX
 CC This sequence represents a novel sucrose binding protein, SBP1 isolated
 CC from glycine max. This protein is used in a method resulting in the
 CC production of a modified plant sucrose binding protein (SBP) which has a
 CC modified amino acid sequence compared to a corresponding wild-type SBP,
 CC and where expression of the modified SBP in a yeast assay system confers
 CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
 CC The products of the invention can be used for producing transgenic plants
 CC which have modified sucrose uptake activity, particularly in developing
 CC seeds. Enhanced sucrose uptake activity in developing seeds may be
 CC desirable where it is an advantage to increase the carbohydrate content
 CC of the seed (e.g. where the seed is the primary plant material harvested,
 CC such as soybean). In contrast, decreased sucrose uptake activity in
 CC seeds might be desirable where the vegetative material of the plant is
 CC harvested. The SBP regulatory regions confer specific or enhanced
 CC expression in developing seeds and so may be used to express any
 CC transgene in developing seeds.
 CC
 CC Sequence 524 AA:
 SQ
 Query Match 25.0%; Score 63; DB 20; Length 524;
 Best Local Similarity 38.2%; Pred. NO. 3.9;
 Matches 13; Conservative 4; Mismatches 15; Indels 2; Gaps 1.
 OY 2 EFDROVEBECKRQCMOLE-TSGQMRRCVSGCDK 33
 I : I I I I I : I I I I I :
 Db 34 eeedpelvtckhqcqgqytlegrkrcvclqscdr 67
 RESULT 14
 ID W90342 standard; protein; 409 AA.
 W90342
 AC W90342:
 XX
 DT 24-MAY-1999 (first entry)
 DE G. max truncated SBP2 protein.
 XX
 KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
 KW seed; carbohydrate content; soybean.
 XX
 OS Glycine max.
 XX
 PN W09853086-A1.
 XX
 PD 26-NOV-1998.
 XX
 PE 21-MAY-1998; 98WO-US10465.
 XX
 PR 22-MAY-1997; 97US-0047568.
 XX
 PA (UNIM) UNIV WASHINGTON STATE RES FOUND.
 XX
 PI Chao WS, Grimes HD;
 XX
 DR WPI: 1999-070155/06.
 XX
 PT New modified plant sucrose binding proteins - used to develop
 PT transgenic plants which can have enhanced or decreased sucrose
 PT uptake activity in developing seeds
 XX
 PS Claim 7; Page 39-40; 58pp; English.
 CC This sequence represents a novel sucrose binding protein, SBP2 isolated
 CC from glycine max. This protein is used in a method resulting in the
 CC production of a modified plant sucrose binding protein (SBP) which has a
 CC modified amino acid sequence compared to a corresponding wild-type SBP,
 CC and where expression of the modified SBP in a yeast assay system confers
 CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
 CC The products of the invention can be used for producing transgenic plants
 CC which have modified sucrose uptake activity, particularly in developing
 CC seeds. Enhanced sucrose uptake activity in developing seeds may be
 CC desirable where it is an advantage to increase the carbohydrate content
 CC of the seed (e.g. where the seed is the primary plant material harvested,
 CC such as soybean). In contrast, decreased sucrose uptake activity in
 CC seeds might be desirable where the vegetative material of the plant is
 CC harvested. The SBP regulatory regions confer specific or enhanced
 CC expression in developing seeds and so may be used to express any
 CC transgene in developing seeds.
 CC
 CC Sequence 524 AA:
 SQ
 Query Match 25.0%; Score 63; DB 20; Length 524;
 Best Local Similarity 38.2%; Pred. NO. 3.9;
 Matches 13; Conservative 4; Mismatches 15; Indels 2; Gaps 1.
 OY 2 EFDROVEBECKRQCMOLE-TSGQMRRCVSGCDK 33
 I : I I I I I : I I I I I :
 Db 34 eeedpelvtckhqcqgqytlegrkrcvclqscdr 67
 RESULT 14
 ID W90342 standard; protein; 409 AA.
 W90342
 AC W90342:
 XX
 DT 24-MAY-1999 (first entry)
 DE G. max truncated SBP2 protein.
 XX
 KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
 KW seed; carbohydrate content; soybean.
 XX
 OS Glycine max.
 XX
 PN W09853086-A1.
 XX
 PD 26-NOV-1998.
 XX
 PE 21-MAY-1998; 98WO-US10465.
 XX
 PR 22-MAY-1997; 97US-0047568.
 XX
 PA (UNIM) UNIV WASHINGTON STATE RES FOUND.
 XX
 PI Chao WS, Grimes HD;
 XX
 DR WPI: 1999-070155/06.
 XX
 PT New modified plant sucrose binding proteins - used to develop
 PT transgenic plants which can have enhanced or decreased sucrose
 PT uptake activity in developing seeds
 XX
 PS Claim 7; Page 39-40; 58pp; English.
 CC This sequence represents a novel sucrose binding protein, SBP2 isolated
 CC from glycine max. This protein is used in a method resulting in the
 CC production of a modified plant sucrose binding protein (SBP) which has a
 CC modified amino acid sequence compared to a corresponding wild-type SBP,
 CC and where expression of the modified SBP in a yeast assay system confers
 CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
 CC The products of the invention can be used for producing transgenic plants
 CC which have modified sucrose uptake activity, particularly in developing
 CC seeds. Enhanced sucrose uptake activity in developing seeds may be
 CC desirable where it is an advantage to increase the carbohydrate content
 CC of the seed (e.g. where the seed is the primary plant material harvested,
 CC such as soybean). In contrast, decreased sucrose uptake activity in
 CC seeds might be desirable where the vegetative material of the plant is
 CC harvested. The SBP regulatory regions confer specific or enhanced
 CC expression in developing seeds and so may be used to express any
 CC transgene in developing seeds.
 CC
 CC Sequence 524 AA:
 SQ
 Query Match 25.0%; Score 63; DB 20; Length 524;
 Best Local Similarity 38.2%; Pred. NO. 3.9;
 Matches 13; Conservative 4; Mismatches 15; Indels 2; Gaps 1.
 OY 2 EFDROVEBECKRQCMOLE-TSGQMRRCVSGCDK 33
 I : I I I I I : I I I I I :
 Db 34 eeedpelvtckhqcqgqytlegrkrcvclqscdr 67
 RESULT 14
 ID W90342 standard; protein; 409 AA.
 W90342
 AC W90342:
 XX
 DT 24-MAY-1999 (first entry)
 DE G. max truncated SBP2 protein.
 XX
 KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
 KW seed; carbohydrate content; soybean.
 XX
 OS Glycine max.
 XX
 PN W09853086-A1.
 XX
 PD 26-NOV-1998.
 XX
 PE 21-MAY-1998; 98WO-US10465.
 XX
 PR 22-MAY-1997; 97US-0047568.
 XX
 PA (UNIM) UNIV WASHINGTON STATE RES FOUND.
 XX
 PI Chao WS, Grimes HD;
 XX
 DR WPI: 1999-070155/06.
 XX
 PT New modified plant sucrose binding proteins - used to develop
 PT transgenic plants which can have enhanced or decreased sucrose
 PT uptake activity in developing seeds
 XX
 PS Claim 7; Page 39-40; 58pp; English.
 CC This sequence represents a novel sucrose binding protein, SBP2 isolated
 CC from glycine max. This protein is used in a method resulting in the
 CC production of a modified plant sucrose binding protein (SBP) which has a
 CC modified amino acid sequence compared to a corresponding wild-type SBP,
 CC and where expression of the modified SBP in a yeast assay system confers
 CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
 CC The products of the invention can be used for producing transgenic plants
 CC which have modified sucrose uptake activity, particularly in developing
 CC seeds. Enhanced sucrose uptake activity in developing seeds may be
 CC desirable where it is an advantage to increase the carbohydrate content
 CC of the seed (e.g. where the seed is the primary plant material harvested,
 CC such as soybean). In contrast, decreased sucrose uptake activity in
 CC seeds might be desirable where the vegetative material of the plant is
 CC harvested. The SBP regulatory regions confer specific or enhanced
 CC expression in developing seeds and so may be used to express any
 CC transgene in developing seeds.
 CC
 CC Sequence 524 AA:
 SQ
 Query Match 25.0%; Score 63; DB 20; Length 524;
 Best Local Similarity 38.2%; Pred. NO. 3.9;
 Matches 13; Conservative 4; Mismatches 15; Indels 2; Gaps 1.
 OY 2 EFDROVEBECKRQCMOLE-TSGQMRRCVSGCDK 33
 I : I I I I I : I I I I I :
 Db 34 eeedpelvtckhqcqgqytlegrkrcvclqscdr 67
 RESULT 14
 ID W90342 standard; protein; 409 AA.
 W90342
 AC W90342:
 XX
 DT 24-MAY-1999 (first entry)
 DE G. max truncated SBP2 protein.
 XX
 KW SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
 KW seed; carbohydrate content; soybean.
 XX
 OS Glycine max.
 XX
 PN W09853086-A1.
 XX
 PD 26-NOV-1998.
 XX
 PE 21-MAY-1998; 98WO-US10465.
 XX
 PR 22-MAY-1997; 97US-0047568.
 XX
 PA (UNIM) UNIV WASHINGTON STATE RES FOUND.
 XX
 PI Chao WS, Grimes HD;
 XX
 DR WPI: 1999-070155/06.
 XX
 PT New modified plant sucrose binding proteins - used to develop
 PT transgenic plants which can have enhanced or decreased sucrose
 PT uptake activity in developing seeds
 XX
 PS Claim 7; Page 39-40; 58pp; English.
 CC This sequence represents a novel sucrose binding protein, SBP2 isolated
 CC from glycine max. This protein is used in a method resulting in the
 CC production of a modified plant sucrose binding protein (SBP) which has a
 CC modified amino acid sequence compared to a corresponding wild-type SBP,
 CC and where expression of the modified SBP in a yeast assay system confers
 CC enhanced sucrose uptake compared to the corresponding wild-type SBP.
 CC The products of the invention can be used for producing transgenic plants
 CC which have modified sucrose uptake activity, particularly in developing
 CC seeds. Enhanced sucrose uptake activity in developing seeds may be
 CC desirable where it is an advantage to increase the carbohydrate content
 CC of the seed (e.g. where the seed is the primary plant material harvested,
 CC such as soybean). In contrast, decreased sucrose uptake activity in
 CC seeds might be desirable where the vegetative material of the plant is
 CC harvested. The SBP regulatory regions confer specific or enhanced
 CC expression in developing seeds and so may be used to express any
 CC transgene in developing seeds.
 CC
 CC Sequence 524 AA:
 SQ
 Query Match 25.0%; Score 63; DB 20; Length 524;
 Best Local Similarity 38.2%; Pred. NO. 3.9;
 Matches 13; Conservative 4; Mismatches 15; Indels 2; Gaps 1.
 OY 2 EFDROVEBECKRQCMOLE-TSGQMRRCVSGCDK 33
 I : I I I I I : I I I I I :
 Db 34 eeedpelvtckhqcqgqytlegrkrcvclqscdr 67
 RESULT 14
 ID W90342 standard; protein; 409 AA.
 W90342
 AC W90342:
 XX
 DT 24-M

CC	modified amino acid sequence compared to a corresponding wild-type SBP,
CC	and where expression of the modified SBP in a yeast assay system confers
CC	enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC	The products of the invention can be used for producing transgenic plants
CC	which have modified sucrose uptake activity, particularly in developing
CC	seeds. Enhanced sucrose uptake activity in developing seeds may be
CC	desirable where it is an advantage to increase the carbohydrate content
CC	of the seed (e.g. where the seed is the primary plant material harvested,
CC	such as soybean). In contrast, decreased sucrose uptake activity in
CC	seeds might be desirable where the vegetative material of the plant is
CC	harvested. The SBP regulatory regions confer specific or enhanced
CC	expression in developing seeds and so may be used to express any
CC	transgene in developing seeds.
CC	
SQ	Sequence 409 AA;
Query Match	24.8%; Score 62.5; DB 20; Length 409;
Best local Similarity	36.6%; Pred. No. 3.5;
Matches 15; Conservative 3; Mismatches 14; Indels 9; Gaps 2	
QY	7 EYECKROCMOLE--TSGMRRRCVSCD-----KRPED 38
Dd	38 elvtckhgqgqrqgyresdkrtclqgcsmkgerexqe 78
RESULT 15	
W90341	
ID	W90341 standard; protein: 489 AA.
XX	
AC	W90341:
XX	
DT	24-MAY-1999 (first entry)
XX	
DE	G. max SBP2 protein.
XX	
KM	SBP1; sucrose binding protein; SBP2; sucrose uptake; transgenic plant;
WM	seed; carbohydrate content; soybean.
KX	
OS	Glycine max.
XX	
PN	W09853086-A1.
PD	
XX	26-NOV-1998.
PF	
XX	21-MAY-1998; 98WO-US10465.
PR	
XX	22-MAY-1997; 97US-0047568.
PA	(UNITM) UNIV WASHINGTON STATE RES FOUND.
XX	
PI	Chao WS, Grimes HD;
DR	WPI; 1999-070155/06.
PT	
XX	New modified plant sucrose binding proteins - used to develop
PT	transgenic plants which can have enhanced or decreased sucrose
PT	uptake activity in developing seeds
XX	
PS	Claim 13b; Page 37-38; 58pp; English.
XX	
CC	This sequence represents a novel sucrose binding protein, SBP2 isolated
CC	from glycine max. This protein is used in a method resulting in the
CC	production of a modified plant sucrose binding protein (SBP) which has a
CC	modified amino acid sequence compared to a corresponding wild-type SBP,
CC	and where expression of the modified SBP in a yeast assay system confers
CC	enhanced sucrose uptake compared to the corresponding wild-type SBP.
CC	The products of the invention can be used for producing transgenic plants
CC	which have modified sucrose uptake activity, particularly in developing
CC	seeds. Enhanced sucrose uptake activity in developing seeds may be
CC	desirable where it is an advantage to increase the carbohydrate content
CC	of the seed (e.g. where the seed is the primary plant material harvested,
CC	such as soybean). In contrast, decreased sucrose uptake activity in

